```
==============================================================
Sequence Listing was accepted.
See attached Validation Report.
If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).
Reviewer: Keisha Douglas
Timestamp: [year=2007; month=12; day=31; hr=11; min=48; sec=34; ms=931;
]
==============================================================
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Application No: 10566944   Version No: 2.1

Input Set:

Output Set:

Started: 2007-12-31 11:47:29.794
Finished: 2007-12-31 11:47:48.193
Elapsed: 0 hr(s) 0 min(s) 18 sec(s) 399 ms
Total Warnings: 108
Total Errors: 281
No. of SeqIDs Defined: 192
Actual SeqID Count: 192

Error code	Error Description
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (1)
E 300	Invalid codon found Ile SEQID (1) POS: 97
E 300	Invalid codon found Glu SEQID (1) POS: 100
E 300	Invalid codon found Asn SEQID (1) POS: 103
E 300	Invalid codon found Tyr SEQID (1) POS: 106
E 300	Invalid codon found Gln SEQID (1) POS: 109
E 300	Invalid codon found Gly SEQID (1) POS: 112
E 300	Invalid codon found Arg SEQID (1) POS: 115
E 300	Invalid codon found Asp SEQID (1) POS: 118
E 300	Invalid codon found Ala SEQID (1) POS: 121
E 300	Invalid codon found Thr SEQID (1) POS: 124
E 300	Invalid codon found Asp SEQID (1) POS: 127
E 300	Invalid codon found Ala SEQID (1) POS: 130
E 300	Invalid codon found Phe SEQID (1) POS: 133
E 300	Invalid codon found Met SEQID (1) POS: 136
E 300	Invalid codon found Val SEQID (1) POS: 139
E 300	Invalid codon found Met SEQID (1) POS: 142
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (1)

```
        Input Set:


        Output Set:



           Started:   2007-12-31 11:47:29.794
          Finished:   2007-12-31 11:47:48.193
           Elapsed:   0 hr(s) 0 min(s) 18 sec(s) 399 ms
    Total Warnings:   108
      Total Errors:   281
No. of SeqIDs Defined:  192
  Actual SeqID Count:   192


Error code      Error Description


E   300    Invalid codon found   Leu SEQID  (1)   POS: 481

E   300    Invalid codon found   Val SEQID  (1)   POS: 484

E   300    Invalid codon found   Gly SEQID  (1)   POS: 487

E   300    Invalid codon found   Leu SEQID  (1)   POS: 490
           This error has occured more than 20 times, will not be displayed

E   355    Empty lines found between the amino acid numbering and the

E   321    No. of Bases conflict, this line has no nucleotides  SEQID (1)

E   355    Empty lines found between the amino acid numbering and the

E   321    No. of Bases conflict, this line has no nucleotides  SEQID (1)

W   402    Undefined organism found in <213>  in SEQ ID (11)

W   402    Undefined organism found in <213>  in SEQ ID (12)

W   402    Undefined organism found in <213>  in SEQ ID (13)

W   402    Undefined organism found in <213>  in SEQ ID (14)

E   355    Empty lines found between the amino acid numbering and the

E   321    No. of Bases conflict, this line has no nucleotides  SEQID (19)

E   355    Empty lines found between the amino acid numbering and the

E   321    No. of Bases conflict, this line has no nucleotides  SEQID (19)

E   355    Empty lines found between the amino acid numbering and the

E   321    No. of Bases conflict, this line has no nucleotides  SEQID (19)

E   355    Empty lines found between the amino acid numbering and the

E   321    No. of Bases conflict, this line has no nucleotides  SEQID (19)

E   336    Empty lines found between the proteins and the dna

E   336    Empty lines found between the proteins and the dna
```

```
          Input Set:


          Output Set:



              Started:   2007-12-31 11:47:29.794
             Finished:   2007-12-31 11:47:48.193
              Elapsed:   0 hr(s) 0 min(s) 18 sec(s) 399 ms
      Total Warnings:    108
        Total Errors:    281
 No. of SeqIDs Defined:  192
    Actual SeqID Count:  192
```

Error code	Error Description
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna This error has occured more than 20 times, will not be displayed
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (26)
W 402	Undefined organism found in <213> in SEQ ID (29)
W 402	Undefined organism found in <213> in SEQ ID (30)

Input Set:

Output Set:

Started:	2007-12-31 11:47:29.794
Finished:	2007-12-31 11:47:48.193
Elapsed:	0 hr(s) 0 min(s) 18 sec(s) 399 ms
Total Warnings:	108
Total Errors:	281
No. of SeqIDs Defined:	192
Actual SeqID Count:	192

Error code	Error Description
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (30)
W 402	Undefined organism found in <213> in SEQ ID (33)
W 402	Undefined organism found in <213> in SEQ ID (34)
W 402	Undefined organism found in <213> in SEQ ID (35)
W 402	Undefined organism found in <213> in SEQ ID (36)
W 402	Undefined organism found in <213> in SEQ ID (41)
W 402	Undefined organism found in <213> in SEQ ID (42)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (42)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (46)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (58)
W 402	Undefined organism found in <213> in SEQ ID (67)
W 402	Undefined organism found in <213> in SEQ ID (68)
W 402	Undefined organism found in <213> in SEQ ID (69)
W 402	Undefined organism found in <213> in SEQ ID (70)
W 402	Undefined organism found in <213> in SEQ ID (71)
W 402	Undefined organism found in <213> in SEQ ID (72)
W 402	Undefined organism found in <213> in SEQ ID (73)
W 402	Undefined organism found in <213> in SEQ ID (74)

This error has occured more than 20 times, will not be displayed

```
        Input Set:


        Output Set:



         Started:   2007-12-31 11:47:29.794
        Finished:   2007-12-31 11:47:48.193
         Elapsed:   0 hr(s) 0 min(s) 18 sec(s) 399 ms
  Total Warnings:   108
    Total Errors:   281
No. of SeqIDs Defined:   192
Actual SeqID Count:   192
```

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (115)
W 213	Artificial or Unknown found in <213> in SEQ ID (116)
W 213	Artificial or Unknown found in <213> in SEQ ID (121)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (121)
W 213	Artificial or Unknown found in <213> in SEQ ID (122)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (122)
W 213	Artificial or Unknown found in <213> in SEQ ID (123)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (123)
W 213	Artificial or Unknown found in <213> in SEQ ID (124)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (124)
W 213	Artificial or Unknown found in <213> in SEQ ID (125)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (125)
W 213	Artificial or Unknown found in <213> in SEQ ID (126)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (126)
W 213	Artificial or Unknown found in <213> in SEQ ID (127)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (127)
W 213	Artificial or Unknown found in <213> in SEQ ID (128)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (128)
W 213	Artificial or Unknown found in <213> in SEQ ID (129)

```
            Input Set:


            Output Set:



            Started:    2007-12-31 11:47:29.794
           Finished:    2007-12-31 11:47:48.193
            Elapsed:    0 hr(s) 0 min(s) 18 sec(s) 399 ms
     Total Warnings:    108
       Total Errors:    281
No. of SeqIDs Defined:  192
  Actual SeqID Count:   192


Error code      Error Description


E  224     <220>,<223> section required as <213> has Artificial sequence or
           Unknown in SEQID (129)

W  213     Artificial or Unknown found in <213>  in SEQ ID (130)

E  224     <220>,<223> section required as <213> has Artificial sequence or
           Unknown in SEQID (130)

W  213     Artificial or Unknown found in <213>  in SEQ ID (139)

W  213     Artificial or Unknown found in <213>  in SEQ ID (140)

W  213     Artificial or Unknown found in <213>  in SEQ ID (141)

W  213     Artificial or Unknown found in <213>  in SEQ ID (142)

W  213     Artificial or Unknown found in <213>  in SEQ ID (143)

E  224     <220>,<223> section required as <213> has Artificial sequence or
           Unknown in SEQID (143)

W  213     Artificial or Unknown found in <213>  in SEQ ID (144)

E  224     <220>,<223> section required as <213> has Artificial sequence or
           Unknown in SEQID (144)

W  213     Artificial or Unknown found in <213>  in SEQ ID (145)

E  224     <220>,<223> section required as <213> has Artificial sequence or
           Unknown in SEQID (145)

W  213     Artificial or Unknown found in <213>  in SEQ ID (146)
            This error has occured more than 20 times, will not be displayed

E  224     <220>,<223> section required as <213> has Artificial sequence or
           Unknown in SEQID (146)

E  224     <220>,<223> section required as <213> has Artificial sequence or
           Unknown in SEQID (147)

E  224     <220>,<223> section required as <213> has Artificial sequence or
           Unknown in SEQID (148)

E  224     <220>,<223> section required as <213> has Artificial sequence or
           Unknown in SEQID (149)
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```
              Input Set:


             Output Set:



                Started:   2007-12-31 11:47:29.794
               Finished:   2007-12-31 11:47:48.193
                Elapsed:   0 hr(s) 0 min(s) 18 sec(s) 399 ms
         Total Warnings:   108
           Total Errors:   281
  No. of SeqIDs Defined:   192
     Actual SeqID Count:   192
```

Error code	Error Description
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (150)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (151)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (152) This error has occured more than 20 times, will not be displayed

<110>   Zank, Thorsten
        Bauer, Jorg
        Cirpus, Petra
        Abbadi, Amine
        Heinz, Ernst
        Qiu, Xiao
        Vrinten, Patricia
        Sperling, Petra
        Domergue, Frederic
        Meyer, Astrid
        Kirsch, Jelena

<120>   METHOD FOR THE PRODUCTION OF MULTIPLE-UNSATURATED FATTY ACIDS IN
        TRANSGENIC ORGANISMS

<130>   12810-00193-US

<140>   10/566,944
<141>   2006-02-01

<150>   DE 103 35 992.3
<151>   2003-08-01

<150>   DE 103 44 557.9
<151>   2003-09-24

<150>   DE 103 47 869.8
<151>   2003-10-10

<150>   DE 103 59 593.7
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<150>   DE 10 2004 009 457.8
<151>   2004-02-27

<150>   DE 10 2004 012 370.5
<151>   2004-03-13

<150>   DE 10 2004 024 014.0
<151>   2004-05-14

<160>   192

<170>   PatentIn version 3.1

<210>   1
<211>   1266
<212>   DNA
<213>   Euglena gracilis

<220>
<221>   CDS
<222>   (1)..(1266)
<223>   delta8-desaturase

<400> 1

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atg aag tca aag cgc caa gcg ctt ccc ctt aca att gat gga aca aca      48
Met Lys Ser Lys Arg Gln Ala Leu Pro Leu Thr Ile Asp Gly Thr Thr
1               5                   10                  15

tat gat gtg tct gcc tgg gtc aat ttc cac cct ggt ggt gcg gaa att      96
Tyr Asp Val Ser Ala Trp Val Asn Phe His Pro Gly Gly Ala Glu Ile
                20                  25                  30

ata gag aat tac caa gga agg gat gcc act gat gcc ttc atg gtt atg     144
Ile Glu Asn Tyr Gln Gly Arg Asp Ala Thr Asp Ala Phe Met Val Met

        35                  40                  45

cac tct caa gaa gcc ttc gac aag ctc aag cgc atg ccc aaa atc aat     192
His Ser Gln Glu Ala Phe Asp Lys Leu Lys Arg Met Pro Lys Ile Asn
    50                  55                  60

ccc agt tct gag ttg cca ccc cag gct gca gtg aat gaa gct caa gag     240
Pro Ser Ser Glu Leu Pro Pro Gln Ala Ala Val Asn Glu Ala Gln Glu
65                  70                  75                  80

gat ttc cgg aag ctc cga gaa gag ttg atc gca act ggc atg ttt gat     288
Asp Phe Arg Lys Leu Arg Glu Glu Leu Ile Ala Thr Gly Met Phe Asp
                85                  90                  95

gcc tcc ccc ctc tgg tac tca tac aaa atc agc acc aca ctg ggc ctt     336
Ala Ser Pro Leu Trp Tyr Ser Tyr Lys Ile Ser Thr Thr Leu Gly Leu
                100                 105                 110

gga gtg ctg ggt tat ttc ctg atg gtt cag tat cag atg tat ttc att     384
Gly Val Leu Gly Tyr Phe Leu Met Val Gln Tyr Gln Met Tyr Phe Ile
            115                 120                 125

ggg gca gtg ttg ctt ggg atg cac tat caa cag atg ggc tgg ctt tct     432
Gly Ala Val Leu Leu Gly Met His Tyr Gln Gln Met Gly Trp Leu Ser
        130                 135                 140

cat gac att tgc cac cac cag act ttc aag aac cgg aac tgg aac aac     480
His Asp Ile Cys His His Gln Thr Phe Lys Asn Arg Asn Trp Asn Asn
145                 150                 155                 160

ctc gtg gga ctg gta ttt ggc aat ggt ctg caa ggt ttt tcc gtg aca     528
Leu Val Gly Leu Val Phe Gly Asn Gly Leu Gln Gly Phe Ser Val Thr

            165                 170                 175

tgc tgg aag gac aga cac aat gca cat cat tcg gca acc aat gtt caa     576
Cys Trp Lys Asp Arg His Asn Ala His His Ser Ala Thr Asn Val Gln
                180                 185                 190

ggg cac gac cct gat att gac aac ctc ccc ctc tta gcc tgg tct gag     624
Gly His Asp Pro Asp Ile Asp Asn Leu Pro Leu Leu Ala Trp Ser Glu
            195                 200                 205

gat gac gtc aca cgg gcg tca ccg att tcc cgc aag ctc att cag ttc     672
```

```
Asp Asp Val Thr Arg Ala Ser Pro Ile Ser Arg Lys Leu Ile Gln Phe
    210                 215             220


cag cag tat tat ttc ttg gtc atc tgt atc ttg ttg cgg ttc att tgg        720
Gln Gln Tyr Tyr Phe Leu Val Ile Cys Ile Leu Leu Arg Phe Ile Trp
225                 230             235             240


tgt ttc cag agc gtg ttg acc gtg cgc agt ctg aag gac aga gat aac        768
Cys Phe Gln Ser Val Leu Thr Val Arg Ser Leu Lys Asp Arg Asp Asn
                245             250             255


caa ttc tat cgc tct cag tat aag aag gag gcc att ggc ctc gcc ctg        816
Gln Phe Tyr Arg Ser Gln Tyr Lys Lys Glu Ala Ile Gly Leu Ala Leu
            260             265             270


cat tgg aca ttg aag gcc ctg ttc cac tta ttc ttt atg ccc agc atc        864
His Trp Thr Leu Lys Ala Leu Phe His Leu Phe Phe Met Pro Ser Ile
        275             280             285


ctc aca tcg ctg ttg gta ttt ttc gtt tcg gag ctg gtt ggc ggc ttc        912
Leu Thr Ser Leu Leu Val Phe Phe Val Ser Glu Leu Val Gly Gly Phe


        290             295             300


ggc att gcg atc gtg gtg ttc atg aac cac tac cca ctg gag aag atc        960
Gly Ile Ala Ile Val Val Phe Met Asn His Tyr Pro Leu Glu Lys Ile
305             310             315             320


ggg gac tcg gtc tgg gat ggc cat gga ttc tcg gtt ggc cag atc cat       1008
Gly Asp Ser Val Trp Asp Gly His Gly Phe Ser Val Gly Gln Ile His
                325             330             335


gag acc atg aac att cgg cga ggg att atc aca gat tgg ttt ttc gga       1056
Glu Thr Met Asn Ile Arg Arg Gly Ile Ile Thr Asp Trp Phe Phe Gly
            340             345             350


ggc ttg aac tac cag atc gag cac cat ttg tgg ccg acc ctc cct cgc       1104
Gly Leu Asn Tyr Gln Ile Glu His His Leu Trp Pro Thr Leu Pro Arg
        355             360             365


cac aac ctg aca gcg gtt agc tac cag gtg gaa cag ctg tgc cag aag       1152
His Asn Leu Thr Ala Val Ser Tyr Gln Val Glu Gln Leu Cys Gln Lys
        370             375             380


cac aac ctg ccg tat cgg aac ccg ctg ccc cat gaa ggg ttg gtc atc       1200
His Asn Leu Pro Tyr Arg Asn Pro Leu Pro His Glu Gly Leu Val Ile
385             390             395             400


ctg ctg cgc tat ctg gcg gtg ttc gcc cgg atg gcg gag aag caa ccc       1248
Leu Leu Arg Tyr Leu Ala Val Phe Ala Arg Met Ala Glu Lys Gln Pro
                405             410             415


gcg ggg aag gct cta taa                                               1266
Ala Gly Lys Ala Leu


        420
```

<210> 2
<211> 421
<212> PRT
<213> Euglena gracilis

<400> 2

Met Lys Ser Lys Arg Gln Ala Leu Pro Leu Thr Ile Asp Gly Thr Thr
1   5   10   15

Tyr Asp Val Ser Ala Trp Val Asn Phe His Pro Gly Gly Ala Glu Ile
            20   25   30

Ile Glu Asn Tyr Gln Gly Arg Asp Ala Thr Asp Ala Phe Met Val Met
            35   40   45

His Ser Gln Glu Ala Phe Asp Lys Leu Lys Arg Met Pro Lys Ile Asn
        50   55   60

Pro Ser Ser Glu Leu Pro Pro Gln Ala Ala Val Asn Glu Ala Gln Glu
65   70   75   80

Asp Phe Arg Lys Leu Arg Glu Glu Leu Ile Ala Thr Gly Met Phe Asp
                85   90   95

Ala Ser Pro Leu Trp Tyr Ser Tyr Lys Ile Ser Thr Thr Leu Gly Leu
            100   105   110

Gly Val Leu Gly Tyr Phe Leu Met Val Gln Tyr Gln Met Tyr Phe Ile
            115   120   125

Gly Ala Val Leu Leu Gly Met His Tyr Gln Gln Met Gly Trp Leu Ser
        130   135   140

His Asp Ile Cys His His Gln Thr Phe Lys Asn Arg Asn Trp Asn Asn
145   150   155   160

Leu Val Gly Leu Val Phe Gly Asn Gly Leu Gln Gly Phe Ser Val Thr
                165   170   175

Cys Trp Lys Asp Arg His Asn Ala His His Ser Ala Thr Asn Val Gln
                180   185   190

```
Gly His Asp Pro Asp Ile Asp Asn Leu Pro Leu Leu Ala Trp Ser Glu
    195             200         205

Asp Asp Val Thr Arg Ala Ser Pro Ile Ser Arg Lys Leu Ile Gln Phe
210             215         220

Gln Gln Tyr Tyr Phe Leu Val Ile Cys Ile Leu Leu Arg Phe Ile Trp
225         230         235             240

Cys Phe Gln Ser Val Leu Thr Val Arg Ser Leu Lys Asp Arg Asp Asn
            245         250             255

Gln Phe Tyr Arg Ser Gln Tyr Lys Lys Glu Ala Ile Gly Leu Ala Leu
            260         265             270

His Trp Thr Leu Lys Ala Leu Phe His Leu Phe Phe Met Pro Ser Ile
    275             280             285

Leu Thr Ser Leu Leu Val Phe Phe Val Ser Glu Leu Val Gly Gly Phe
    290             295             300

Gly Ile Ala Ile Val Val Phe Met Asn His Tyr Pro Leu Glu Lys Ile
305             310             315             320

Gly Asp Ser Val Trp Asp Gly His Gly Phe Ser Val Gly Gln Ile His
            325             330             335

Glu Thr Met Asn Ile Arg Arg Gly Ile Ile Thr Asp Trp Phe Phe Gly
            340             345             350

Gly Leu Asn Tyr Gln Ile Glu His His Leu Trp Pro Thr Leu Pro Arg
    355             360             365

His Asn Leu Thr Ala Val Ser Tyr Gln Val Glu Gln Leu Cys Gln Lys
    370             375             380

His Asn Leu Pro Tyr Arg Asn Pro Leu Pro His Glu Gly Leu Val Ile
385             390             395             400

Leu Leu Arg Tyr Leu Ala Val Phe Ala Arg Met Ala Glu Lys Gln Pro
            405             410             415

Ala Gly Lys Ala Leu
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<210> 3
<211> 777
<212> DNA
<213> Isochrysis galbana

<220>
<221> CDS
<222> (1)..(777)
<223> delta9-elongase

<400> 3
atg gcc ctc gca aac gac gcg gga gag cgc atc tgg gcg gct gtg acc   48
Met Ala Leu Ala Asn Asp Ala Gly Glu Arg Ile Trp Ala Ala Val Thr
1   5   10   15

gac ccg gaa atc ctc att ggc acc ttc tcg tac ttg cta ctc aaa ccg   96
Asp Pro Glu Ile Leu Ile Gly Thr Phe Ser Tyr Leu Leu Leu Lys Pro
                20   25   30

ctg ctc cgc aat tcc ggg ctg gtg gat gag aag aag ggc gca tac agg   144
Leu Leu Arg Asn Ser Gly Leu Val Asp Glu Lys Lys Gly Ala Tyr Arg
        35   40   45

acg tcc atg atc tgg tac aac gtt ctg ctg gcg ctc ttc tct gcg ctg   192
Thr Ser Met Ile Trp Tyr Asn Val Leu Leu Ala Leu Phe Ser Ala Leu
    50   55   60

agc ttc tac gtg acg gcg acc gcc ctc ggc tgg gac tat ggt acg ggc   240
Ser Phe Tyr Val Thr Ala Thr Ala Leu Gly Trp Asp Tyr Gly Thr Gly
65   70   75   80

gcg tgg ctg cgc agg caa acc ggc gac aca ccg cag ccg ctc ttc cag   288
Ala Trp Leu Arg Arg Gln Thr Gly Asp Thr Pro Gln Pro Leu Phe Gln
                85   90   95

tgc ccg tcc ccg gtt tgg gac tcg aag ctc ttc aca tgg acc gcc aag   336
Cys Pro Ser Pro Val Trp Asp Ser Lys Leu Phe Thr Trp Thr Ala Lys
                100   105   110

gca ttc tat tac tcc aag tac gtg gag tac ctc gac acg gcc tgg ctg   384
Ala Phe Tyr Tyr Ser Lys Tyr Val Glu Tyr Leu Asp Thr Ala Trp Leu
        115   120   125

agg gtc tcc ttt ctc cag gcc ttc cac cac ttt ggc gcg ccg tgg gat   432
Arg Val Ser Phe Leu Gln Ala Phe His His Phe Gly Ala Pro Trp Asp
    130   135   140

gtg tac ctc ggc att cgg ctg cac aac gag ggc gta tgg atc ttc atg   480
Val Tyr Leu Gly Ile Arg Leu His Asn Glu Gly Val Trp Ile Phe Met
145   150   155   160

ttt ttc aac tcg ttc att cac acc atc atg tac acc tac tac ggc ctc   528
Phe Phe Asn Ser Phe Ile His Thr Ile Met Tyr Thr Tyr Tyr Gly Leu
                165   170   175

```
acc gcc gcc ggg tat aag ttc aag gcc aag ccg ctc atc acc gcg atg       576
Thr Ala Ala Gly Tyr Lys Phe Lys Ala Lys Pro Leu Ile Thr Ala Met
            180                 185                 190

cag atc tgc cag ttc gtg ggc ggc ttc ctg ttg gtc tgg gac tac atc       624
Gln Ile Cys Gln Phe Val Gly Gly Phe Leu Leu Val Trp Asp Tyr Ile
            195                 200                 205

aac gtc ccc tgc ttc aac tcg gac aaa ggg aag ttg ttc agc tgg gct       672
Asn Val Pro Cys Phe Asn Ser Asp Lys Gly Lys Leu Phe Ser Trp Ala
     210                 215                 220

ttc aac tat gca tac gtc ggc tcg gtc ttc ttg ctc ttc tgc cac ttt       720
Phe Asn Tyr Ala Tyr Val Gly Ser Val Phe Leu Leu Phe Cys His Phe
225                 230                 235                 240

ttc tac cag gac aac ttg gca acg aag aaa tcg gcc aag gcg ggc aag       768
Phe Tyr Gln Asp Asn Leu Ala Thr Lys Lys Ser Ala Lys Ala Gly Lys
                245                 250                 255

cag ctc tag                                                            777
Gln Leu
```

```
Met Ala Leu Ala Asn Asp Ala Gly Glu Arg Ile Trp Ala Ala Val Thr
1               5                   10                  15


Asp Pro Glu Ile Leu Ile Gly Thr Phe Ser Tyr Leu Leu Leu Lys Pro
            20                  25                  30


Leu Leu Arg Asn Ser Gly Leu Val Asp Glu Lys Lys Gly Ala Tyr Arg
            35                  40                  45


Thr Ser Met Ile Trp Tyr Asn Val Leu Leu Ala Leu Phe Ser Ala Leu
    50                  55                  60


Ser Phe Tyr Val Thr Ala Thr Ala Leu Gly Trp Asp Tyr Gly Thr Gly
65                  70                  75                  80


Ala Trp Leu Arg Arg Gln Thr Gly Asp Thr Pro Gln Pro Leu Phe Gln
                85                  90                  95
```

Cys Pro Ser Pro Val Trp Asp Ser Lys Leu Phe Thr Trp Thr Ala Lys
            100   105   110

Ala Phe Tyr Tyr Ser Lys Tyr Val Glu Tyr Leu Asp Thr Ala Trp Leu
        115   120   125

Arg Val Ser Phe Leu Gln Ala Phe His His Phe Gly Ala Pro Trp Asp
    130   135   140

Val Tyr Leu Gly Ile Arg Leu His Asn Glu Gly Val Trp Ile Phe Met
145   150   155   160

Phe Phe Asn Ser Phe Ile His Thr Ile Met Tyr Thr Tyr Tyr Gly Leu
                165   170   175

Thr Ala Ala Gly Tyr Lys Phe Lys Ala Lys Pro Leu Ile Thr Ala Met
                180   185   190

Gln Ile Cys Gln Phe Val Gly Gly Phe Leu Leu Val Trp Asp Tyr Ile
        195   200   205

Asn Val Pro Cys Phe Asn Ser Asp Lys Gly Lys Leu Phe Ser Trp Ala
    210   215   220

Phe Asn Tyr Ala Tyr Val Gly Ser Val Phe Leu Leu Phe Cys His Phe
225   230   235   240

Phe Tyr Gln Asp Asn Leu Ala Thr Lys Lys Ser Ala Lys Ala Gly Lys
                245   250   255

Gln Leu

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atg gct ccg gat gcg gat aag ctt cga caa cgc cag acg act gcg gta      48
Met Ala Pro Asp Ala Asp Lys Leu Arg Gln Arg Gln Thr Thr Ala Val
1               5                   10                  15

gcg aag cac aat gct gct acc ata tcg acg cag gaa cgc ctt tgc agt      96
Ala Lys His Asn Ala Ala Thr Ile Ser Thr Gln Glu Arg Leu Cys Ser
                20                  25                  30

ctg tct tcg ctc aaa ggc gaa gaa gtc tgc atc gac gga atc atc tat     144
Leu Ser Ser Leu Lys Gly Glu Glu Val Cys Ile Asp Gly Ile Ile Tyr
        35                  40                  45

gac ctc caa tca ttc gat cat ccc ggg ggt gaa acg atc aaa atg ttt     192
Asp Leu Gln Ser Phe Asp His Pro Gly Gly Glu Thr Ile Lys Met Phe
        50                  55                  60

ggt ggc aac gat gtc act gta cag tac aag atg att cac ccg tac cat     240
Gly Gly Asn Asp Val Thr Val Gln Tyr Lys Met Ile His Pro Tyr His
65                  70                  75                  80

acc gag aag cat ttg gaa aag atg aag cgt gtc ggc aag gt
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